SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
              Tang, Y. Tom
              Corley, Neil C.
              Guegler, Karl J.
              Yue, Henry
              Patterson, Chandra

(ii) TITLE OF THE INVENTION: PROTEINS ASSOCIATED WITH EGF SIGNALING

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:
   (A) ADDRESSEE: Incyte Genomics, Inc.
   (B) STREET: 3160 Porter Dr.
   (C) CITY: Palo Alto
   (D) STATE: CA
   (E) COUNTRY: USA
   (F) ZIP: 94304

(v) COMPUTER READABLE FORM:
   (A) MEDIUM TYPE: Diskette
   (B) COMPUTER: IBM Compatible
   (C) OPERATING SYSTEM: DOS
   (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:
   (A) APPLICATION NUMBER: To Be Assigned
   (B) FILING DATE: Herewith

(vii) PRIOR APPLICATION DATA:
   (A) APPLICATION NUMBER: 09/069,725
   (B) FILING DATE: April 29, 1998

(viii) ATTORNEY/AGENT INFORMATION:
   (A) NAME: Billings, Lucy J.
   (B) REGISTRATION NUMBER: 36,749
   (C) REFERENCE/DOCKET NUMBER: PF-0515-1 CON

(ix) TELECOMMUNICATION INFORMATION:
   (A) TELEPHONE: 650-855-0555
   (B) TELEFAX: 650-845-4166

   (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 298 amino acids
   (B) TYPE: amino acid
   (C) STRANDEDNESS: single
   (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
   (A) LIBRARY: COLNNOT16
   (B) CLONE: 1281694

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Asn Asp Ser Leu Arg Thr Asp Val Phe Val Arg Phe Gln Pro Glu
1   5   10   15

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Ser Ile Ala Cys Ala Cys Ile Tyr Leu Ala Ala Arg Thr Leu Glu Ile
              20                      25                  30
Pro Leu Pro Asn Arg Pro His Trp Phe Leu Leu Phe Gly Ala Thr Glu
              35                      40                  45
Glu Glu Ile Gln Glu Ile Cys Leu Lys Ile Leu Gln Leu Tyr Ala Arg
         50                      55                  60
Lys Lys Val Asp Leu Thr His Leu Glu Gly Glu Val Glu Leu Lys Arg Lys
65                      70                  75                  80
His Ala Ile Glu Glu Ala Lys Ala Gln Ala Arg Gly Leu Leu Pro Gly
                   85                      90                  95
Gly Thr Gln Val Leu Asp Gly Thr Ser Gly Phe Ser Pro Ala Pro Lys
              100                     105                 110
Leu Val Glu Ser Pro Lys Glu Gly Lys Gly Ser Lys Pro Ser Pro Leu
              115                     120                 125
Ser Val Lys Asn Thr Lys Arg Arg Leu Glu Gly Ala Lys Lys Ala Lys
         130                     135                 140
Ala Asp Ser Pro Val Asn Gly Leu Pro Lys Gly Arg Glu Ser Arg Ser
145                     150                     155                 160
Arg Ser Arg Ser Arg Glu Gln Ser Tyr Ser Arg Ser Pro Arg Ser
              165                     170                 175
Ala Ser Pro Lys Arg Arg Lys Ser Asp Ser Gly Ser Thr Ser Gly Gly
              180                     185                 190
Ser Lys Ser Gln Ser Arg Ser Arg Ser Arg Ser Asp Ser Pro Pro Arg
              195                     200                 205
Gln Ala Pro Arg Ser Ala Pro Tyr Lys Gly Ser Glu Ile Arg Gly Ser
         210                     215                 220
Arg Lys Ser Lys Asp Cys Lys Tyr Pro Gln Lys Pro His Lys Ser Arg
225                     230                     235                 240
Ser Arg Ser Ser Ser Arg Ser Arg Ser Arg Ser Arg Glu Arg Ala Asp
                   245                     250                 255
Asn Pro Gly Lys Tyr Lys Lys Lys Ser His Tyr Tyr Arg Asp Gln Arg
         260                     265                 270
Arg Glu Arg Ser Arg Ser Tyr Glu Arg Thr Gly Arg Arg Tyr Glu Arg
    275                     280                     285
Asp His Pro Gly His Ser Arg His Arg Arg
290                     295
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 3464 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single
      (D) TOPOLOGY: linear

    (vii) IMMEDIATE SOURCE:
      (A) LIBRARY: COLNNOT16
      (B) CLONE: 1281694

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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TTCGTGAAGC ACTCCATGGA GCATGTGTCA ATGGCCTGTG TCCACCTGGC TTCCAAGATA    60
GAAGAGGCCC CAAGACGCAT ACGGGACGTC ATCAATGTGT TTCACCGCCT TCGACAGCTG   120
AGAGACAAAA AATAATCGTT ATGTACCTTC AGGTGTTAGA GTGTGAGCGT AACCAACACC   180
TGGTCCAGAC CTCATGGGTA GCCTCTGAGG GTAAGTGACT AAGACTTCTC CTCTGCTGTC   240
CAAGCGCTTT GGTGCAGGGA CAGCGGCATC TTCAGCCAAT CCAGTGCAGG CTCTCCACCG   300
AAGGCTGGCT CTAGACTGGT GACCCCTTGT TGAAATGGGA CGGCTCTGAT   360
GAGCCCGAGA AGAGGCCTGC CCTTGGGTGC GGAGTCTCCC TCCGCACGAT GCTCCCACGC   420
GTCCAACTTG CACCCAAGGG GCTTTTCCCT CTTCCAAGTG GACTCCTTCA AGGAAGCTGC   480
AGCTCGGTCA GCAGAGAAGG GGCTGCCGC CAGCGCCCTG GAGGAAGAGG AAGAGGAACC   540
CAAGAGGATG GCTTGTCTCC CAGCAGCCAC ACCGGCTTTG TGCTCAGCCA GTTCATTTGA   600
GTTTGCATGT TTCTCTGCAC TATGGATTTT GAGCATTTAG ATTTCTTTAA TCAAAAGCGT   660
TTTAGTGACT CCAGTAGACA TTTTCTTTCT GAGGCATCGT GCTTTGCATG AGAGCAGGCC   720
AAGGTTGAGG GGAAAAGTAA AGTTAAAGTC GGTTCTCTTT CATAGCAACA CGTATTGTCT   780
GACATTCAGC CAGCTTTTTT TTTTTCTAAT AATTTCTGTG CCTTTCTGTC CTGTATTTAC   840
TGTATTTAGA AAAAGCAGCT AGAATATTTC TCCATTAACT CTTGAGATTC ACAGGACTGT   900
```

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```
CTAGCTCTGA GTCCTAGCAA TAGACTCCTT AGAGGAGTAG TACGTTTATC TAGATTTTCT    960
CTAGATAATG CAGGCGGAAG ACCTGGGTTC CCGGGTGGGG CATTGCAGTT CTTCCTGTGT   1020
TTGGCTTCCA GGAATTACAT GAACGACAGC CTTCGCACCG ACGTCTTCGT GCGGTTCCAG   1080
CCAGAGAGCA TCGCCTGTGC CTGCATTTAT CTTGCTGCCC GGACGCTGGA GATCCCTTTG   1140
CCCAATCGTC CCCATTGGTT TCTTTTGTTT GGAGCAACTG AAGAAGAAAT TCAGGAAATC   1200
TGCTTAAAGA TCTTGCAGCT TTATGCTCGG AAAAAGGTTG ATCTCACACA CCTGGAGGGT   1260
GAAGTGGAAA AAAGAAAGCA CGCTATCGAA GAGGCAAAGG CCCAAGCCCG GGGCCTGTTG   1320
CCTGGGGGCA CACAGGTGCT GGATGGTACC TCGGGGTTCT CTCCTGCCCC CAAGCTGGTG   1380
GAATCCCCCA AAGAAGGTAA AGGGAGCAAG CCTTCCCCAC TGTCTGTGAA GAACACCAAG   1440
AGGAGGCTGG AGGGCGCCAA GAAAGCCAAG GCGGACAGCC CCGTGAACGG CTTGCCAAAG   1500
GGGCGAGAGA GTCGGAGTCG GAGCCGGAGC CGTGAGCAGA GCTACTCGAG GTCCCCATCC   1560
CGATCAGCGT CTCCTAAGAG GAGGAAAAGT GACAGCGGCT CCACATCTGG TGGGTCCAAG   1620
TCGCAGAGCC GCTCCCGGAG CAGGAGTGAC TCCCCACCGA GACAGGCCCC CCGCAGCGCT   1680
CCCTACAAAG GCTCTGAGAT TCGGGGCTCC CGGAAGTCCA AGGACTGCAA GTACCCCCAG   1740
AAGCCACACA AGTCTCGGAG CCGGAGTTCT TCCCGTTCTC GAAGCAGGTC ACGGGAGCGG   1800
GCGGATAATC CGGGAAAATA CAAGAAGAAA AGTCATTACT ACAGAGATCA GCGACGAGAG   1860
CGCTCGAGGT CGTATGAACG CACAGGCCGT CGCTATGAGC GGGACCACCC TGGGCACAGC   1920
AGGCATCGGA GGTGAGGCGG GGTTGCAGTG ACTGGTGGCC GCAAGCCCTT CCCTGGGGAG   1980
TACCTGATGG CTGCCCTTTG ACCCCCGGTG GCTGCCCTTT GACCCCCGGG TGTGCTCTCA   2040
GCGCAAGTGG TCCTAGAACA GGATTCTTTT TGGAAATGCT TGTCGACTGG ACCTTGGTGG   2100
ATTTGGAAAT GGAACTGAGG GACCGGTGAC ACGTGCTTCA GACCGGTCTG GGGTGCGGCG   2160
CACACCTGGG CCCGTGCAGG GCTCAGCTCG GCAGCAGCTC TGAGGGCAGC TCAATGAAAA   2220
AGTGAATGCA CACGCCCTTG TTGGCGTGGC CTGGCATGGC CTGGTGCTAT CGGCAGCCGC   2280
TCTCCACTCC CCGACTGATA CTCAATTACG TGAAGCCAAG AAAGATGATT TTTAGAACCT   2340
TTGCCTATAT TAGGTTGTAC TTATGTACAT ATTTTGCAGT GTTTCACAGG AGAAAGTGGC   2400
CTTAACTGCC TCCCTGCTGT TCTCCACGTT GTAAATAAAC ATGTGTTTAA TACAAGTTAA   2460
AGCTATGTAT GAAAACTCAG AACTTGAATC CCGTCAGCTT AAAACTTGTG TAGGGAATCC   2520
TGACTTTTAA AATGTGAGGG TATTTGGATC TGTGTTGAAA GTCGTATATT TTTATCTGTG   2580
CGGTGCTGAG TGCAGGCCAC CAGCTCCTAA ATAGAGGTTC CCTATATGCG CGTATGACAT   2640
GGTGAATAAA CACAACTCTC TCCACTCAGG ACATCCGGAG CGTTATGGAC GTGGTAGGTG   2700
GTCGTTCTGT GTGCTTGTGA AAGTGTCCAG GCGTGTGCAC AGCCAGTGCG CCCACTTCCG   2760
GGCTCCTTGC TCCCTGCTGT ACTGAAGTTT TGGATTTTGC ATCCAATCCT GTGTGCCTGC   2820
CCTTCTGCCG AAGCTTGTGA GGGGCCTGAG TCCTCTGCCC ATCAGGATGA CAGGCTCCTT   2880
CCTGCAGGGC CATAGGAGGG AAGTTTTGGA AACACAGAAT GATTCCAAGG TGCTCTCGTT   2940
CCTGAGGGGG ACTGGTTTGT AACCCATGAC ATCTGTGGGC GAGAGAGGCA GCTGGGAGCA   3000
GGACACTTGG AGGGTCACCC CACGGGGGTG GCACCTGCAC TCTGAGTGCC CCCCACTGTC   3060
ATCAGCTGCC TCTTACCGTG GACACAGTTT TGGTTTTGGG GACTAGGGGG CCCCACTCCT   3120
GGTGGTACCG TTTGGACTTA CTAGGGCAGT GGGCACATATA GGCCGGGGGCT AGTGGGATAA   3180
CGGGGAGTTA CGCCTGATGA CTTTTTTGAT GGAATCCTGC ATTAGATAGC TGGTGGGACC   3240
CCCCCCTCAG AATTGGGGAA CTGAGGGAGAC TCCAGGGAGG GTGTCCTTCC AGGGAGGAGCA   3300
GCTATGAGGG GCCCCCTAGC TTCCTGTGCC TGGAAGTAAG AGAACCAGTA AAGGGCCATA   3360
CACACCTGTA CCCAAGAGAC CGCTCTCCAT TTGCTTTCTT TTTTTACTAA ATAATTGTAA   3420
AATATTATTA TGACATAAAG AACCATTTAA GGCCAAAAAA AAAA                    3464
```

(2) INFORMATION FOR SEQ ID NO:3:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 332 amino acids
     (B) TYPE: amino acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (vii) IMMEDIATE SOURCE:
     (A) LIBRARY: BEPINOT01
     (B) CLONE: 2056178

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Tyr Ser Ala Gln Arg Phe Trp Gly Thr Ile Trp Ala Arg Arg Gly
1               5                   10                  15
Ala His Leu Ala Pro Pro Asp Ala Ser Ile Leu Ile Ser Asn Val Cys
        20                  25                  30
Ser Ile Gly Asp His Val Ala Gln Glu Leu Phe Gln Gly Ser Asp Leu
        35                  40                  45
Gly Met Ala Glu Glu Ala Glu Arg Pro Gly Glu Lys Ala Gly Gln His
    50                  55                  60
Ser Pro Leu Arg Glu Glu His Val Thr Cys Val Ser Ile Leu Asp
65                  70                  75                  80
Glu Phe Leu Gln Thr Tyr Gly Ser Leu Ile Pro Leu Ser Thr Asp Glu
                85                  90                  95
Val Val Glu Lys Leu Glu Asp Ile Phe Gln Gln Glu Phe Ser Thr Pro
            100                 105                 110
Ser Arg Lys Gly Leu Val Leu Gln Leu Ile Gln Ser Tyr Gln Arg Met
        115                 120                 125
Pro Gly Asn Ala Met Val Arg Gly Phe Arg Val Ala Tyr Lys Arg His
        130                 135                 140
Val Leu Thr Met Asp Asp Leu Gly Thr Leu Tyr Gly Gln Asn Trp Leu
145                 150                 155                 160
Asn Asp Gln Val Met Asn Met Tyr Gly Asp Leu Val Met Asp Thr Val
                165                 170                 175
Pro Glu Lys Val His Phe Phe Asn Ser Phe Phe Tyr Asp Lys Leu Arg
            180                 185                 190
Thr Lys Gly Tyr Asp Gly Val Lys Arg Trp Thr Lys Asn Val Asp Ile
        195                 200                 205
Phe Asn Lys Gly Glu Leu Leu Leu Ile Pro Ile His Leu Glu Val His Trp
        210                 215                 220
Ser Leu Ile Ser Val Asp Val Arg Arg Arg Thr Ile Thr Tyr Phe Asp
225                 230                 235                 240
Ser Gln Arg Thr Leu Asn Arg Arg Cys Pro Lys His Ile Ala Lys Tyr
            245                 250                 255
Leu Gln Ala Glu Val Lys Lys Asp Arg Leu Asp Phe His Gln Gly
        260                 265                 270
Trp Lys Gly Tyr Phe Lys Met Asn Val Ala Arg Gln Asn Asn Asp Ser
    275                 280                 285
Asp Cys Gly Ala Phe Val Leu Gln Tyr Cys Lys His Leu Ala Leu Ser
    290                 295                 300
Gln Pro Phe Ser Phe Thr Gln Gln Asp Met Pro Lys Leu Arg Arg Gln
305                 310                 315                 320
Ile Tyr Lys Glu Leu Cys His Cys Lys Leu Thr Val
                325                 330
```

   (2) INFORMATION FOR SEQ ID NO:4:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 1991 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: single
     (D) TOPOLOGY: linear

   (vii) IMMEDIATE SOURCE:

(A) LIBRARY: BEPINOT01
(B) CLONE: 2056178

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
GCCTCCCTGT CCCCCGACCC TCTTTTGATG CCTCAGCAAG TGAAGAGGAG GAAGAAGAGG     60
AGGAGGAGGA GGATGAAGAT GAAGAGGAGG AAGTGGCAGC TTGGAGGCTG CCCCCAAGAT    120
GGAGTCAGCT GGGAACCTCC CAGCGGCCCC GCCCTTCCCG CCCCACTCAT CGAAAAACCT    180
GCTCACAGCG CCGCCGCCGA GCCATGAGAG CCTTCCGGAT GCTGCTCTAC TCAAAAAGCA    240
CCTCGCTGAC ATTCCACTGG AAGCTTTGGG GGCGCCACCG GGGCCGGCGG CGGGGCCTCG    300
CACACCCCAA GAACCATCTT TCACCCCAGC AAGGGGGTGC GACGCCACAG GTGCCATCCC    360
CCTGTTGTCG TTTTGACTCC CCCCGGGGGC CACCTCCACC CCGGCTGGGT CTGCTAGGTG    420
CTCTCATGGC TGAGGATGGG GTGAGAGGGT CTCCACCAGT GCCCTCTGGG CCCCCCATGG    480
AGGAAGATGG ACTCAGGTGG ACTCCAAAGT CTCCTCTGGA CCCTGACTCG GGCCTCCTTT    540
CATGTACTCT GCCCAACGGT TTTGGGGGAC AATCTGGGCC AGAAGGGGAG CGCACTTGGC    600
ACCCCCTGAT GCCAGCATCC TCATCAGCAA TGTGTGCAGC ATGGGGACC ATGTGGCCCA    660
GGAGCTTTTT CAGGGCTCAG ATTTGGGCAT GGCAGAAGAG GCAGAGAGGC CTGGGGAGAA    720
AGCCGGCCAG CACAGCCCCC TGCGAGAGGA GCATGTGACC TGCGTACAGA GCATCTTGGA    780
CGAATTCCTT CAAACGTATG GCAGCCTCAT ACCCCTCAGC ACTGATGAGG TAGTAGAGAA    840
GCTGGAGGAC ATTTTCCAGC AGGAGTTTTC CACCCGTTCC AGGAAGGGCC TGGTGTTGCA    900
GCTGATCCAG TCTTACCAGC GGATGCCAGG CAATGCCATG GTGAGGGGCT TCCGAGTGGC    960
TTATAAGCGG CACGTGCTGA CCATGGATGA CTTGGGGACC TTGTATGGAC AGAACTGGCT   1020
CAATGACCAG GTGATGAACA TGTATGGAGA CCTGGTCATG GACACAGTCC CTGAAAAGGT   1080
GCATTTCTTC AATAGTTTCT TCTATGATAA ACTCCGTACC AAGGGTTATG ATGGGGTGAA   1140
AAGGTGGACC AAAAACGTGG ACATCTTCAA TAAGGAGCTA CTGCTAATCC CCATCCACCT   1200
GGAGGTGCAT TGGTCCCTCA TCTCTGTTGA TGTGAGGCGA CGCACCATCA CCTATTTTGA   1260
CTCGCAGCGT ACCCTAAACC GCCGCTGCCC TAAGCATATT GCCAAGTATC TACAGGCAGA   1320
GGCGGTAAAG AAAGACCGAC TGGATTTCCA CCAGGGCTGG AAAGGTTACT TCAAAATGAA   1380
TGTGGCCAGG CAGAATAATG ACAGTGACTG TGGTGCTTTT GTGTTGCAGT ACTGCAAGCA   1440
TCTGGCCCTG TCTCAGCCAT TCAGCTTCAC CCAGCAGGAC ATGCCCAAAC TTCGTCGGCA   1500
GATCTACAAG GAGCTGTGTC ACTGCAAACT CACTGTGTGA GCCTCGTACC CCAGACCCCA   1560
AGCCCATAAA TGGGAAGGGA GACATGGGAG TCCCTTCCCA AGAAACTCCA GTTCCTTTCC   1620
TCTCTTGCCT CTTCCCACTC ACTTCCCTTT GGTTTTTCAT ATTTAAATGT TTCAATTTCT   1680
GTATTTTTTT TTCTTTGAGA GAATACTTGT TGATTTCTGA TGTGCAGGGG GTGGCTACAG   1740
AAAAGCCCCT TTCTTCCTCT GTTTGCAGGG GAGTGTGGCC CTGTGGCCTG GGTGGAGCAG   1800
TCATCCTCCC CCTTCCCCGT GCAGGGAGCA GGAAATCAGT GCTGGGGGTG GTGGGCGGAC   1860
AATAGGATCA CTGCCTGCCA GATCTTCAAA CTTTTATATA TATATATATA TATATATATA   1920
TATATATATA TATATATATA TATATATATA AATATATAAA TGCCACGGTC CTGCTCTGGT   1980
CAATAAAGAT C                                                       1991
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 186 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:
(A) LIBRARY: GenBank
(B) CLONE: 1276645

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Met Glu Gly Pro Lys Lys Ala Gln Gly His Ser Pro Val Asn Gly Leu
1               5                   10                  15
Leu Lys Gly Gln Glu Ser Arg Ser Gln Ser Arg Ser Arg Glu Gln Ser
                20                  25                  30
Tyr Ser Arg Ser Pro Ser Arg Ser Ala Ser Pro Lys Arg Arg Lys Ser
            35                  40                  45
Asp Ser Gly Ser Thr Ser Gly Gly Ser Lys Ser Gln Ser Arg Ser Arg
        50                  55                  60
Ser Arg Ser Asp Ser Pro Pro Arg Gln Val His Arg Gly Ala Pro Tyr
65                  70                  75                  80
Lys Gly Ser Glu Val Arg Gly Ser Arg Lys Ser Lys Asp Cys Lys Tyr
                85                  90                  95
```

```
Leu Thr Gln Lys Pro His Lys Ser Arg Ser Arg Ser Ser Ser Arg Ser
            100                     105                 110
Arg Ser Arg Ser Arg Glu Arg Thr Asp Asn Ser Gly Lys Tyr Lys Lys
        115                     120                 125
Lys Ser His Tyr Tyr Arg Asp Gln Arg Arg Glu Arg Ser Arg Ser Tyr
    130                     135                 140
Glu Arg Thr Gly His Arg Tyr Glu Arg Asp His Pro Gly His Ser Arg
145                     150                     155             160
His Arg Arg Cys Asp Arg Ile Ser Gly Gly Cys Pro Trp Ser Leu Pro
                165                     170                 175
Val Gly His Thr Leu Ala Ser Val Ala Leu
            180                     185
```